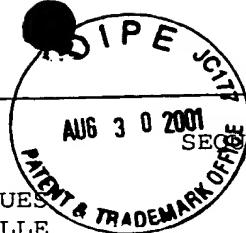


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Ser Val Thr Gly Leu Asp Glu Val Pro Phe Lys Gly Glu Lys Val Lys  
340 345 350

Leu Val Arg Leu Arg Asn Pro Trp Gly Gln Val Glu Trp Asn Gly Ser  
355 360 365

Trp Ser Asp Arg Trp Lys Asp Trp Ser Phe Val Asp Lys Asp Glu Lys  
370 375 380

Ala Arg Leu Gln His Gln Val Thr Glu Asp Gly Glu Phe Trp Met Ser  
385 390 395 400

Tyr Glu Asp Phe Ile Tyr His Phe Thr Lys Leu Glu Ile Cys Asn Leu  
405 410 415

Thr Ala Asp Ala Leu Gln Ser Asp Lys Leu Gln Thr Trp Thr Val Ser  
420 425 430

Val Asn Glu Gly Arg Trp Val Arg Gly Cys Ser Ala Gly Gly Cys Arg  
435 440 445

Asn Phe Pro Asp Thr Phe Trp Thr Asn Pro Gln Tyr Arg Leu Lys Leu  
450 455 460

Leu Glu Glu Asp Asp Asp Pro Asp Asp Ser Glu Val Ile Cys Ser Phe



465                      470                      475                      480  
 Leu Val Ala Leu Met Gln Lys Asn Arg Arg Lys Asp Arg Lys Leu Gly  
                                  485                      490                      495  
 Ala Ser Leu Phe Thr Ile Gly Phe Ala Ile Tyr Glu Val Pro Lys Glu  
                                  500                      505                      510  
 Met His Gly Asn Lys Gln His Leu Gln Lys Asp Phe Phe Leu Tyr Asn  
                                  515                      520                      525  
 Ala Ser Lys Ala Arg Ser Lys Thr Tyr Ile Asn Met Arg Glu Val Ser  
                                  530                      535                      540  
 Gln Arg Phe Arg Leu Pro Pro Ser Glu Tyr Val Ile Val Pro Ser Thr  
                                  545                      550                      555                      560  
 Tyr Glu Pro His Gln Glu Gly Glu Phe Ile Leu Arg Val Phe Ser Glu  
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 Lys Arg Asn Leu Ser Glu Glu Val Glu Asn Thr Ile Ser Val Asp Arg  
                                  580                      585                      590  
 Pro Val Lys Lys Lys Lys Thr Lys Pro Ile Ile Phe Val Ser Asp Arg  
                                  595                      600                      605  
 Ala Asn Ser Asn Lys Glu Leu Gly Val Asp Gln Glu Ser Glu Glu Gly  
                                  610                      615                      620  
 Lys Gly Lys Thr Ser Pro Asp Lys Gln Lys Gln Ser Pro Gln Pro Gln  
                                  625                      630                      635                      640  
 Pro Gly Ser Ser Asp Gln Glu Ser Glu Glu Gln Gln Gln Phe Arg Asn  
                                  645                      650                      655  
 Ile Phe Lys Gln Ile Ala Gly Asp Asp Met Glu Ile Cys Ala Asp Glu  
                                  660                      665                      670  
 Leu Lys Lys Val Leu Asn Thr Val Val Asn Lys His Lys Asp Leu Lys  
                                  675                      680                      685  
 Thr His Gly Phe Thr Leu Glu Ser Cys Arg Ser Met Ile Ala Leu Met  
                                  690                      695                      700  
 Asp Thr Asp Gly Ser Gly Lys Leu Asn Leu Gln Glu Phe His His Leu  
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 Trp Asn Lys Ile Lys Ala Trp Gln Lys Ile Phe Lys His Tyr Asp Thr  
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 Asp Gln Ser Gly Thr Ile Asn Ser Tyr Glu Met Arg Asn Ala Val Asn  
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 Asp Ala Gly Phe His Leu Asn Asn Gln Leu Tyr Asp Ile Ile Thr Met  
                                  755                      760                      765  
 Arg Tyr Ala Asp Lys His Met Asn Ile Asp Phe Asp Ser Phe Ile Cys  
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Pro Arg Ser Pro Gly Pro Val Pro His Pro Ala Gln Gly Lys Thr Thr  
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Glu Ala Gly Gly Gly His Pro Gly Gly Ile Tyr Ser Ala Ile Ile Ser  
35 40 45

Arg Asn Phe Pro Ile Ile Gly Val Lys Glu Lys Thr Phe Glu Gln Leu  
50 55 60

His Lys Lys Cys Leu Glu Lys Lys Val Leu Tyr Leu Asp Pro Glu Phe  
 65 70 75 80  
 Pro Pro Asp Glu Thr Ser Leu Phe Tyr Ser Gln Lys Phe Pro Ile Gln  
 85 90 95  
 Phe Val Trp Lys Arg Pro Pro Glu Ile Cys Glu Asn Pro Arg Phe Ile  
 100 105 110  
 Ile Gly Gly Ala Asn Arg Thr Asp Ile Cys Gln Gly Asp Leu Gly Asp  
 115 120 125  
 Cys Trp Leu Leu Ala Ala Ile Ala Cys Leu Thr Leu Asn Glu Arg Leu  
 130 135 140  
 Leu Phe Arg Val Ile Pro His Asp Gln Ser Phe Thr Glu Asn Tyr Ala  
 145 150 155 160  
 Gly Ile Phe His Phe Gln Phe Trp Arg Tyr Gly Asp Trp Val Asp Val  
 165 170 175  
 Val Ile Asp Asp Cys Leu Pro Thr Tyr Asn Asn Gln Leu Val Phe Thr  
 180 185 190  
 Lys Ser Asn His Arg Asn Glu Phe Trp Ser Ala Leu Leu Glu Lys Ala  
 195 200 205  
 Tyr Ala Lys Leu His Gly Ser Tyr Glu Ala Leu Lys Gly Gly Asn Thr  
 210 215 220  
 Thr Glu Ala Met Glu Asp Phe Thr Gly Gly Val Thr Glu Phe Phe Glu  
 225 230 235 240  
 Ile Lys Asp Ala Pro Ser Asp Met Tyr Lys Ile Met Arg Lys Ala Ile  
 245 250 255  
 Glu Arg Gly Ser Leu Met Gly Cys Ser Ile Asp Asp Gly Thr Asn Met  
 260 265 270  
 Thr Tyr Gly Thr Ser Pro Ser Gly Leu Asn Met Gly Glu Leu Ile Ala  
 275 280 285  
 Arg Met Val Arg Asn Met Asp Asn Ser Leu Leu Arg Asp Ser Asp Leu  
 290 295 300  
 Asp Pro Arg Ala Ser Asp Asp Arg Pro Ser Arg Thr Ile Val Pro Val  
 305 310 315 320  
 Gln Tyr Glu Thr Arg Met Ala Cys Gly Leu Val Arg Gly His Ala Tyr  
 325 330 335  
 Ser Val Thr Gly Leu Glu Glu Ala Leu Phe Lys Gly Glu Lys Val Lys  
 340 345 350  
 Leu Val Arg Leu Arg Asn Pro Trp Gly Gln Val Glu Trp Asn Gly Ser  
 355 360 365  
 Trp Ser Asp Gly Trp Lys Asp Trp Ser Phe Val Asp Lys Asp Glu Lys  
 370 375 380

Ala Arg Leu Gln His Gln Val Thr Glu Asp Gly Glu Phe Trp Met Ser  
 385 390 395 400  
 Tyr Asp Asp Phe Val Tyr His Phe Thr Lys Leu Glu Ile Cys Asn Leu  
 405 410 415  
 Thr Ala Asp Ala Leu Glu Ser Asp Lys Leu Gln Thr Trp Thr Val Ser  
 420 425 430  
 Val Asn Glu Gly Arg Trp Val Arg Gly Cys Ser Ala Gly Gly Cys Arg  
 435 440 445  
 Asn Phe Pro Asp Thr Phe Trp Thr Asn Pro Gln Tyr Arg Leu Lys Leu  
 450 455 460  
 Leu Glu Glu Asp Asp Asp Pro Asp Asp Ser Glu Val Ile Cys Ser Phe  
 465 470 475 480  
 Leu Val Ala Leu Met Gln Lys Asn Arg Arg Lys Asp Arg Lys Leu Gly  
 485 490 495  
 Ala Asn Leu Phe Thr Ile Gly Phe Ala Ile Tyr Glu Val Pro Lys Glu  
 500 505 510  
 Met His Gly Asn Lys Gln His Leu Gln Lys Asp Phe Phe Leu Tyr Asn  
 515 520 525  
 Ala Ser Lys Ala Arg Ser Lys Thr Tyr Ile Asn Met Arg Glu Val Ser  
 530 535 540  
 Gln Arg Phe Arg Leu Pro Pro Ser Glu Tyr Val Ile Val Pro Ser Thr  
 545 550 555 560  
 Tyr Glu Pro His Gln Glu Gly Glu Phe Ile Leu Arg Val Phe Ser Glu  
 565 570 575  
 Lys Arg Asn Leu Ser Glu Glu Ala Glu Asn Thr Ile Ser Val Asp Arg  
 580 585 590  
 Pro Val Lys Lys Lys Lys Asn Lys Pro Ile Ile Phe Val Ser Asp Arg  
 595 600 605  
 Ala Asn Ser Asn Lys Glu Leu Gly Val Asp Gln Glu Ala Glu Glu Gly  
 610 615 620  
 Lys Asp Lys Thr Gly Pro Asp Lys Gln Gly Glu Ser Pro Gln Pro Arg  
 625 630 635 640  
 Pro Gly His Thr Asp Gln Glu Ser Glu Glu Gln Gln Gln Phe Arg Asn  
 645 650 655  
 Ile Phe Arg Gln Ile Ala Gly Asp Asp Met Glu Ile Cys Ala Asp Glu  
 660 665 670  
 Leu Lys Asn Val Leu Asn Thr Val Val Asn Lys His Lys Asp Leu Lys  
 675 680 685  
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 20 25 30  
 Glu Ala Gly Gly Gly Asn Pro Ser Gly Ile Tyr Ser Ala Ile Ile Ser  
 35 40 45  
 Arg Asn Phe Pro Ile Ile Gly Val Lys Glu Lys Thr Phe Glu Gln Leu  
 50 55 60  
 His Lys Lys Cys Leu Glu Lys Lys Val Leu Tyr Val Asp Pro Glu Phe  
 65 70 75 80  
 Pro Pro Asp Glu Thr Ser Leu Phe Tyr Ser Gln Lys Phe Pro Ile Gln  
 85 90 95  
 Phe Val Trp Lys Arg Pro Pro Glu Ile Cys Glu Asn Pro Arg Phe Ile  
 100 105 110  
 Ile Asp Gly Ala Asn Arg Thr Asp Ile Cys Gln Gly Glu Leu Gly Asp  
 115 120 125  
 Cys Trp Phe Leu Ala Ala Ile Ala Cys Leu Thr Leu Asn Gln His Leu  
 130 135 140  
 Leu Phe Arg Val Ile Pro His Asp Gln Ser Phe Ile Glu Asn Tyr Ala  
 145 150 155 160  
 Gly Ile Phe His Phe Gln Phe Trp Arg Tyr Gly Glu Trp Val Asp Val  
 165 170 175  
 Val Ile Asp Asp Cys Leu Pro Thr Tyr Asn Asn Gln Leu Val Phe Thr  
 180 185 190  
 Lys Ser Asn His Arg Asn Glu Phe Trp Ser Ala Leu Leu Glu Lys Ala  
 195 200 205  
 Tyr Ala Lys Leu His Gly Ser Tyr Glu Ala Leu Lys Gly Gly Asn Thr  
 210 215 220  
 Thr Glu Ala Met Glu Asp Phe Thr Gly Gly Val Ala Glu Phe Phe Glu  
 225 230 235 240  
 Ile Arg Asp Ala Pro Ser Asp Met Tyr Lys Ile Met Lys Lys Ala Ile  
 245 250 255  
 Glu Arg Gly Ser Leu Met Gly Cys Ser Ile Asp Asp Gly Thr Asn Met  
 260 265 270  
 Thr Tyr Gly Thr Ser Pro Ser Gly Leu Asn Met Gly Asp Leu Ile Ala

275                      280                      285  
 Arg Met Val Arg Asn Met Glu Asn Ser Arg Leu Arg Asp Ser Ile Leu  
 290                      295                      300  
 Asp Pro Glu Val Ser Asp Asp Arg Pro Thr Arg Thr Ile Val Pro Val  
 305                      310                      315                      320  
 Gln Phe Glu Thr Arg Met Ala Cys Gly Leu Val Arg Gly His Ala Tyr  
 325                      330                      335  
 Ser Val Thr Gly Leu Glu Glu Ala Leu Phe Lys Gly Glu Lys Val Lys  
 340                      345                      350  
 Leu Val Arg Leu Arg Asn Pro Trp Gly Gln Val Glu Trp Asn Gly Ser  
 355                      360                      365  
 Trp Ser Asp Ser Trp Lys Asp Trp Ser Phe Val Asp Lys Asp Glu Lys  
 370                      375                      380  
 Ala Arg Leu Gln His Gln Val Thr Glu Asp Gly Glu Phe Trp Met Ser  
 385                      390                      395                      400  
 Tyr Asp Asp Phe Ile Tyr His Phe Thr Lys Leu Glu Ile Cys Asn Leu  
 405                      410                      415  
 Thr Ala Asp Ala Leu Glu Ser Asp Lys Leu Gln Thr Trp Thr Val Ser  
 420                      425                      430  
 Val Asn Glu Gly Arg Trp Val Arg Gly Cys Ser Ala Gly Thr Gly Arg  
 435                      440                      445  
 Asn Phe Pro Asp Thr Phe Trp Thr Asn Pro Gln Tyr Arg Leu Lys Leu  
 450                      455                      460  
 Leu Glu Glu Asp Asp Asp Pro Asp Asp Ser Glu Val Ile Cys Ser Phe  
 465                      470                      475                      480  
 Leu Val Ala Leu Met Gln Arg Asn Arg Arg Lys Asp Arg Lys Leu Gly  
 485                      490                      495  
 Ala Asn Leu Phe Thr Ile Gly Phe Ala Ile Tyr Glu Val Pro Lys Glu  
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 Met His Gly Asn Lys Gln His Leu Gln Lys Asp Phe Phe Leu Tyr Asn  
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 Ala Ser Lys Ala Arg Ser Arg Thr Tyr Ile Asn Met Arg Glu Val Ser  
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 Glu Arg Phe Arg Leu Pro Pro Ser Glu Tyr Val Ile Val Pro Ser Thr  
 545                      550                      555                      560  
 Tyr Glu Pro His Gln Glu Gly Glu Phe Met Leu Arg Val Phe Ser Glu  
 565                      570                      575  
 Lys Arg Lys Leu Ser Glu Glu Val Glu Asn Thr Ile Ser Val Asp Arg  
 580                      585                      590  
 Pro Val Arg Lys Lys Lys Thr Lys Pro Ile Ile Phe Val Ser Asp Arg  
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Ala Asn Ser Asn Lys Glu Leu Gly Val Asp Gln Glu Ser Glu Glu Gly  
 610 615 620  
 Gln Asp Lys Thr Ser Pro Asp Lys Gln Glu Lys Ser Pro Lys Pro Glu  
 625 630 635 640  
 Pro Ser Asn Thr Asp Gln Glu Ser Glu Glu Gln Gln Gln Phe Arg Asn  
 645 650 655  
 Ile Phe Lys Gln Ile Ala Gly Asp Asp Met Glu Ile Cys Ala Asp Glu  
 660 665 670  
 Leu Lys Lys Val Leu Asn Thr Val Val Asn Lys His Lys Asp Leu Lys  
 675 680 685  
 Thr His Gly Phe Thr Leu Glu Ser Cys Arg Ser Met Ile Ala Leu Met  
 690 695 700  
 Asp Thr Asp Gly Ser Gly Lys Leu Asn Leu Gln Glu Phe His His Leu  
 705 710 715 720  
 Trp Asn Lys Ile Lys Ala Trp Gln Lys Ile Phe Lys His Tyr Asp Thr  
 725 730 735  
 Asp Gln Ser Gly Thr Ile Asn Ser Tyr Glu Met Arg Asn Ala Val Asn  
 740 745 750  
 Asp Ala Gly Phe His Leu Asn Asn Gln Leu Tyr Asp Ile Ile Thr Met  
 755 760 765  
 Arg Tyr Ala Asp Lys His Met Asn Ile Asp Phe Asp Ser Phe Ile Cys  
 770 775 780  
 Cys Phe Val Arg Leu Glu Gly Met Phe Arg Ala Phe His Ala Phe Asp  
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 Lys Asp Gly Asp Gly Ile Ile Lys Leu Asn Val Leu Glu Trp Leu Gln  
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 Leu Thr Met Tyr Ala  
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	Pro	Arg	Ser	Pro	Gly	Pro	Val	Pro	His	Pro	Ala	Gln	Ser	Lys	Ala	Thr
				20					25					30		
Glu	Ala	Gly	Gly	Gly	Asn	Pro	Ser	Gly	Ile	Tyr	Ser	Ala	Ile	Ile	Ser	
		35					40					45				
Arg	Asn	Phe	Pro	Ile	Ile	Gly	Val	Lys	Glu	Lys	Thr	Phe	Glu	Gln	Leu	
	50					55					60					
His	Lys	Lys	Cys	Leu	Glu	Lys	Lys	Val	Leu	Tyr	Val	Asp	Pro	Glu	Phe	
65					70					75					80	
Pro	Pro	Asp	Glu	Thr	Ser	Leu	Phe	Tyr	Ser	Gln	Lys	Phe	Pro	Ile	Gln	
				85					90					95		
Phe	Val	Trp	Lys	Arg	Pro	Pro	Glu	Ile	Cys	Glu	Asn	Pro	Arg	Phe	Ile	
			100					105					110			
Ile	Asp	Gly	Ala	Asn	Arg	Thr	Asp	Ile	Cys	Gln	Gly	Glu	Leu	Gly	Asp	
		115					120					125				
Cys	Trp	Phe	Leu	Ala	Ala	Ile	Ala	Cys	Leu	Thr	Leu	Asn	Gln	His	Leu	
	130					135					140					
Leu	Phe	Arg	Val	Ile	Pro	His	Asp	Gln	Ser	Phe	Ile	Glu	Asn	Tyr	Ala	
145					150					155					160	
Gly	Ile	Phe	His	Phe	Gln	Phe	Trp	Arg	Tyr	Gly	Glu	Trp	Val	Asp	Val	
				165					170					175		

Val Ile Asp Asp Cys Leu Pro Thr Tyr Asn Asn Gln Leu Val Phe Thr  
 180 185 190  
 Lys Ser Asn His Arg Asn Glu Phe Trp Ser Ala Leu Leu Glu Lys Ala  
 195 200 205  
 Tyr Ala Lys Leu His Gly Ser Tyr Glu Ala Leu Lys Gly Gly Asn Thr  
 210 215 220  
 Thr Glu Ala Met Glu Asp Phe Thr Gly Gly Val Ala Glu Phe Phe Glu  
 225 230 235 240  
 12 Ile Arg Asp Ala Pro Ser Asp Met Tyr Lys Ile Met Lys Lys Ala Ile  
 245 250 255  
 Glu Arg Gly Ser Leu Met Gly Cys Ser Ile Asp Asp Gly Thr Asn Met  
 260 265 270  
 Thr Tyr Gly Thr Ser Pro Ser Gly Leu Asn Met Gly Glu Leu Ile Glu  
 275 280 285  
 Arg Met Val Arg Asn Met Asp Asn Ser Arg Leu Arg Asp Ser Ile Leu  
 290 295 300  
 Asp Pro Glu Val Ser Asp Asp Arg Pro Thr Arg Met Ile Val Pro Val  
 305 310 315 320  
 Gln Phe Glu Thr Arg Met Ala Cys Gly Leu Val Arg Gly His Ala Tyr  
 325 330 335  
 Ser Val Thr Gly Leu Glu Glu Ala Leu Tyr Lys Gly Glu Lys Val Lys  
 340 345 350  
 Leu Val Arg Leu Arg Asn Pro Trp Gly Gln Val Glu Trp Asn Gly Ser  
 355 360 365  
 Trp Ser Asp Ser Trp Lys Asp Trp Ser Tyr Val Asp Lys Asp Glu Lys  
 370 375 380  
 Ala Arg Leu Gln His Gln Val Thr Glu Asp Gly Glu Phe Trp Met Ser  
 385 390 395 400  
 Tyr Glu Asp Phe Ile Tyr His Phe Thr Lys Leu Glu Ile Cys Asn Leu  
 405 410 415  
 Thr Ala Asp Ala Leu Gln Ser Asp Lys Leu Gln Thr Trp Thr Val Ser  
 420 425 430  
 Val Asn Glu Gly Arg Trp Val Arg Gly Cys Ser Ala Gly Gly Cys Arg  
 435 440 445  
 Asn Phe Pro Asp Thr Phe Trp Thr Asn Pro Gln Tyr Arg Leu Lys Leu  
 450 455 460  
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 465 470 475 480  
 Leu Val Ala Leu Met Gln Lys Asn Arg Arg Lys Asp Arg Lys Leu Gly  
 485 490 495

Ala Ser Leu Phe Thr Ile Gly Phe Ala Ile Tyr Glu Val Pro Lys Glu  
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 Ala Ser Lys Ala Arg Ser Lys Thr Tyr Ile Asn Met Arg Glu Val Ser  
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 545 550 555 560  
 Tyr Glu Pro His Gln Glu Gly Glu Phe Ile Leu Arg Val Phe Ser Glu  
 565 570 575  
 Lys Arg Asn Leu Ser Glu Glu Val Glu Asn Thr Ile Ser Val Asp Arg  
 580 585 590  
 Pro Val Lys Lys Lys Lys Thr Lys Pro Ile Ile Phe Val Ser Asp Arg  
 595 600 605  
 Ala Asn Ser Asn Lys Glu Leu Gly Val Asp Gln Glu Ser Glu Glu Gly  
 610 615 620  
 Lys Gly Lys Thr Ser Pro Asp Lys Gln Lys Gln Ser Pro Gln Pro Gln  
 625 630 635 640  
 Pro Gly Ser Ser Asp Gln Glu Ser Glu Glu Gln Gln Gln Phe Arg Asn  
 645 650 655  
 Ile Phe Lys Gln Ile Ala Gly Asp Asp Met Glu Ile Cys Ala Asp Glu  
 660 665 670  
 Leu Lys Lys Val Leu Asn Thr Val Val Asn Lys His Lys Asp Leu Lys  
 675 680 685  
 Thr His Gly Phe Thr Leu Glu Ser Cys Arg Ser Met Ile Ala Leu Met  
 690 695 700  
 Asp Thr Asp Gly Ser Gly Lys Leu Asn Leu Gln Glu Phe His His Leu  
 705 710 715 720  
 Trp Asn Lys Ile Lys Ala Trp Gln Lys Ile Phe Lys His Tyr Asp Thr  
 725 730 735  
 Asp Gln Ser Gly Thr Ile Asn Ser Tyr Glu Met Arg Asn Ala Val Asn  
 740 745 750  
 Asp Ala Gly Phe His Leu Asn Asn Gln Leu Tyr Asp Ile Ile Thr Met  
 755 760 765  
 Arg Tyr Ala Asp Lys His Met Asn Ile Asp Phe Asp Ser Phe Ile Cys  
 770 775 780  
 Cys Phe Val Arg Leu Glu Gly Met Phe Arg Ala Phe His Ala Phe Asp  
 785 790 795 800  
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 Leu Thr Met Tyr Ala

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22

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19

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<210> 25  
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<400> 25  
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<210> 26  
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<400> 26  
gaggaatgtg gaggaaggac 20

<210> 27  
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<400> 27  
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<210> 28  
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<400> 28  
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<210> 29  
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<400> 29  
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<210> 30  
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<210> 31  
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<400> 31  
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<210> 32  
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<400> 32  
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<210> 33  
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<400> 33  
agcacgaaaa gcaaagataa a

21

<210> 34  
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<400> 34  
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<210> 35  
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<400> 35  
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<400> 36  
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<400> 37

ctctcttccc cacccttacc

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<210> 38

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<223> /label= Table 3

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 <222> (1)..(21)  
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21

<210> 43  
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<210> 44  
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<210> 47  
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gacaaaactcc tgggaagcct

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<223> /label= Table 3

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tgtggatttg tgtgctacgc

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<212> DNA

<213> Homo sapiens

<220>

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<222> (1)..(21)

<223> /label= Table 3

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*ff* <210> 62  
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<400> 62  
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gggaaaacat gcaccttctt

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tagggggtaa aatggaggag

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32 <400> 66  
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<210> 67  
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<400> 67  
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19

<210> 68  
 <211> 1302  
 <212> DNA  
 <213> Homo sapiens

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 <222> (1)..(1302)  
 <223> /note= Flanking 5' genomic region of the sequence of the human nCL1 cDNA described in Figure 2a

<220>  
 <221> misc\_feature  
 <222> (-477)..(-472)  
 <223> /note= Putative Sp1 in Figure 2a

<220>  
 <221> misc\_feature  
 <222> (-364)..(-343)  
 <223> /note= MEF2 binding sites in Figure 2a

<220>  
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 <222> (-685)..(-672)  
 <223> /note= CArG box in Figure 2a

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 ttaagacgga gtctctttct gtcacctggg ctggagtgca gtggcgtgat ctgggttcac 180  
 tacaacctct cctcctctggg ttcaagcaat tcttctgtct cagcctccca agtagctggg 240  
 attacaggca ccccccgcca caccgggctt atttttgtat ttttagtaga gacagggttt 300  
 cactattggt gtccatgctg gtctcgaaact cgtgacctca tgtgatccac ccgcctcggc 360

ctcccaaagt gcagagatta gagacgtgat ccacatggcc cagcaggacc acttttttagc 420  
 agattcagtc ccagtggttca ttttgtggat ggggagagac aagaggtggc aaggtcaagt 480  
 gtgcaggtag agacagggat tttctcaaat gaggactctg ctgagtagca ttttccatgc 540  
 agacattttcc aatgagcgct gacccaagaa catttctaaaa aagataccaa atctaacatt 600  
 gaataatggt ctgatatacct aaaatttttag gactaaaaat catgttctctt aaaattcaca 660  
 gaatattttt gtagaattca gtacctcccg ttcaccctaa ctagcttttt tgcaatattg 720  
 ttttccattc atttgatggc cagtagttgg gtggtctgta taactgccta ctcaataaca 780  
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 atgcagtctc tcttgctctc ataactcacag tgtttcttca catctatttt tagttttcct 960  
 ggctcaagca tcttcaggcc actgaaacac aacctcact ctctttctct ctccctctgg 1020  
 catgcatgct gctggttaga gaccccaag tcaacattgc ttcagaaatc ctttagcact 1080  
 catttctcag gagaacttat ggcttcagaa tcacagctcg gtttttaaga tggacataac 1140  
 ctgtccgacc ttctgatggg ctttcaactt tgaactggat gtggacactt ttctctcaga 1200  
 tgacagaatt actccaactt cccctttgca gttgcttctt ttccttgaag gtagctgtat 1260  
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<210> 69

<211> 1381

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)..(1381)

<223> /note= Flanking 3' genomic region of the sequence of the human nCL1 cDNA described in Figure 2c

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 gttctctctc catttttacc cctacccatc cttgatcggt catgcctagc ctgacccttt 192  
 agtaaagcaa tgaggttaga agaacaaacc cttgtccctt tgccatgtgg aggaaagtgc 252  
 ctgcctctgg tccgagccgc ctcggttctg aagcgagtgc tctgtcttac cttgtcttag 312  
 gctgtctgca gaagcacctg ccggtggcac tcagcacctc cttgtgctag agccctccat 372  
 caccttcacg ctgtccacc atggggccagg aaccaaacca gcaactgggt ctactgctgt 432  
 ggggtaaact aactcagtgg aatagggtg gttactttgg gctgtccaac tcataagttt 492  
 ggctgcattt tgaaaaaagc tgatctaaat aaaggcatgt gtatggctgg tcccttctgt 552  
 ttttgttgtc tcacatttag atatcagcca tgcagtactg aatggcttcc aatcatatac 612  
 tcacctatca cctacaagag aacaatgaaa aacacacaca aaaacaaaat cttgaatttt 672  
 gtaatcatgc ctattgctat ttcttgagca taagaatggc tcagatactt tccaagacat 732  
 aaaaggaagg cagaggaata gttgttgctg taaaagacat caagaataaa tgggtcatgt 792  
 acaacgggag gggccgggta cctgaataat ggagtggaga ttgagctatc ctagctcctc 852  
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 aataggagaa agattttcaa cagcttttcc tccttgacct cctcctttcc caatttatatt 1332  
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